

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: February 1, 2005, 13:07:33 ; Search time 161.5 Seconds
(without alignments)
4125.597 Million cell updates/sec

Title: US-10-659-782A-11
Perfect score: 1030
Sequence: 1 actctggatgggtgctgttt.....tggcagcagggaggggtgggg 579

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO spool_p/US10659782/runat_01022005_130352_14253/app_query.fasta_1.775
-DB=UniProt_02 -OFMT=fastan -SUFFIX=runat -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10659782 @cgn_1_1_244 @runat_01022005_130352_14253 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match %	Length	ID	Description
1	326	31.7	91	Q86YP8	Q86YP8 homo sapien
2	326	31.7	117	GHRL HUMAN	Q9ub03 homo sapien
3	308	29.9	117	Q6UDE7	Q6ude7 macaca mula
4	308	29.9	117	AAQ74381	AAQ74381 macaca mu
5	308	29.9	117	AAQ74837	AAQ74837 macaca mu
6	255	25.7	117	Q8CH53	Q8ch53 meriones un
7	257	25.0	86	Q811T4	Q811t4 mus musculus
8	257	25.0	117	GHRL MOUSE	Q9eqx0 mus musculus
9	256	24.9	117	GHRL RAT	Q9qy7 rattus norv
10	237	23.0	117	GHRL CANFA	Q9b5f8 canis fam
11	237	23.0	117	BAC75929	Bac75929 canis fam
12	232.5	22.6	118	GHRL FIG	Q9gky5 sus scrofa
13	209.5	20.3	116	GHRL BOVIN	Q9bdj6 bos taurus
14	206.5	20.0	116	Q863I0	Q863i0 ovine aries
15	182.5	17.7	65	Q6TGF0	Q6tgf0 sus scrofa
16	182.5	17.7	65	AAQ97622	AAQ97622 sus scrofa

17	162.5	15.8	97	2	Q863C6	Q863c6 ovine aries
18	158.5	15.4	78	2	Q7SD1	Q7ted1 mus musculus
19	147	14.3	54	2	Q6SLG1	Q6slg1 capra hircu
20	147	14.3	54	2	AA67351	AA67351 capra hir
21	146	14.2	54	2	Q6SLF6	Q6slf6 cervus elap
22	146	14.2	54	2	AA67355	AA67355 cervus el
23	145	14.1	52	2	Q6SLF9	Q6slf9 odocoileus
24	145	14.1	52	2	AA67361	AA67361 odocoileu
25	145	14.1	54	2	Q6SLF2	Q6slf2 odocoileus
26	145	14.1	54	2	Q6SLF8	Q6slf8 rangifer ta
27	145	14.1	54	2	AA67353	AA67353 rangifer
28	145	14.1	54	2	AA67359	AA67359 odocoileu
29	142	13.8	54	2	Q6SLF4	Q6slf4 alces alces
30	142	13.8	54	2	AA67357	AA67357 alces alc
31	133	12.9	54	2	Q6SLG3	Q6slg3 ovine aries
32	133	12.9	54	2	AA67349	AA67349 ovine arie
33	130	12.6	54	2	Q6SPC2	Q6spc2 bison bison
34	130	12.6	54	2	AA610495	AA610495 bison bis
35	126.5	12.3	54	2	Q6SLG5	Q6slg5 kogia brevi
36	126.5	12.3	54	2	Q6SLG7	Q6slg7 bos taurus
37	126.5	12.3	54	2	AA67345	AA67345 bos tauru
38	126.5	12.3	54	2	AA67347	AA67347 kogia bre
39	112	10.9	213	2	Q6YWA5	Q6ywa5 oryza sativ
40	112	10.9	213	2	BAD17581	BAD17581 oryza sat
41	112	10.5	262	2	Q6ZMW4	Q6znm4 homo sapien
42	112	10.5	262	2	BAC85372	BAC85372 homo sapi
43	112	10.9	1255	1	MUC1 HUMAN	PI5941 h mucin 1 p
44	110.5	10.7	550	2	Q6SPE9	Q6spe9 oryctolagus
45	110.5	10.7	550	2	AA624088	AA624088 oryctolag

ALIGNMENTS

RESULT 1
Q86YP8 PRELIMINARY; PRT; 91 AA.
AC Q86YP8;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Exon 3-deleted preproghrelin variant.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeffery P.L., Herington A.C., Chopin L.K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY184207; AA027351.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016608; P:growth hormone-releasing hormone activity; IEA.
DR GO; GO:0050791; P:regulation of physiological process; IEA.
DR InterPro; IPR006738; motifin ghrel.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04644; Motilin_ghrel; 1.
DR PRINTS; PR01624; GHRELIN.
SQ SEQUENCE 91 AA; 9972 MW; E7E532D32A3F8609 CRC64;

Alignment Scores:
Pred. No.: 1,928-18 Length: 91
Score: 326.00 Matches: 74
Percent Similarity: 53.19% Conservative: 1
Best Local Similarity: 52.48% Mismatches: 1
Query Match: 31.65% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q86YP8 (1-91)

Qy 112 ATGCGCTCCCGAGGACCGCTCTGAGCCCTCTGCGCATGCTCTGGCTGACTTG 171
|||||
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuApleu 20
|||||


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or send an email to license@sib.ch).
CC -----
CC EMBL; AB029434; BAA83371.1; -
DR EMBL; AB035700; BAB19045.1; -
DR EMBL; AJ252278; CAB65733.1; -
DR EMBL; AF296558; AAG10300.1; -
DR EMBL; AY359053; AAO89412.1; -
DR EMBL; BC025791; AAH25791.1; -
DR PIR; A59316; A59316.
DR MIM; 605353; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0005131; F:growth hormone receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Alternative splicing; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23
FT PEPTIDE 24 51 Ghrelin.
FT PROPEP 52 117 Removed in mature form.
FT LIPID 26 26 O-octanoyl serine.
FT VARSPIC 37 37 Missing (in isoform 2).
FT CONFLICT 72 72 /FTID=VSP_003245.
FT SEQUENCE 117 AA; 12911 MW; 39C0572EBECA2755 CRC64;

Alignment Scores:
Pred. No.: 1.96e-18 Length: 117
Score: 326.00 Matches: 74
Percent Similarity: 53.19% Conservative: 1
Best Local Similarity: 52.48% Mismatches: 0
Query Match: 31.65% Indels: 66
DB: 1 Gaps: 1

US-10-659-782A-11 (1-579) x GHRL_HUMAN (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCCTCTGCTCGGATGCTCTGGCTGACTTG 171
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 172 GCCATGGCAGGCTCCAGCTTCTGAGCCTTGAACACAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 232 CACAAGGCCCAATGTTGTTCCAGCCTGCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db 37 ----- 37
QY 292 CAGCAGGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGTCTGAC 351
Db 37 ----- 37
QY 352 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACACAGACTGTTTCCCCCTTCC 411
Db 37 ----- 37
QY 412 AGCAGAGAAAGAGTCTGAAGAGCCACCAAGCTGCAGCCCGAGCTCTAGCAGGCT 471
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56
QY 472 GCCTCCGCCCGAAGATGAGGTCAAGCAAGAGGGGCGAGAGATGAACCTGGAAGTCCGG 530
Db 56 rpLeuArgProGluAspGlyGlyGlnAlaGluGlyAlaGluAspGluLeuValArg 75

RESULT 3
Q6UDE7

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ID Q6UDE7 PRELIMINARY; PRT; 117 AA.
AC Q6UDE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ghrelin.
GN Name=GHRL;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]_
RP SEQUENCE FROM N.A.
RX PubMed14736731;
RA Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
RA Suomi S., Hansen B.C.;
RT "Characterization of the rhesus monkey ghrelin gene and factors
RT influencing ghrelin gene expression and fasting plasma levels.";
RL Endocrinology 145:2197-2205(2004).
DR EMBL; AY372274; AAQ74837.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
SQ SEQUENCE 117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;

Alignment Scores:
Pred. No.: 6.06e-17 Length: 117
Score: 308.00 Matches: 70
Percent Similarity: 51.06% Conservative: 2
Best Local Similarity: 49.65% Mismatches: 3
Query Match: 29.90% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q6UDE7 (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCCTCTGCTCGGATGCTCTGGCTGACTTG 171
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 172 GCCATGGCAGGCTCCAGCTTCTGAGCCTTGAACACAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg--Ala----- 35
QY 232 CACAAGGCCCAATGTTGTTCCAGCCTGCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACACAGACTGTTTCCCCCTTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAAGAGTCTGAAGAGCCACCAAGCTGCAGCCCGAGCTCTAGCAGGCT 471
Db 36 InGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56
QY 472 GCCTCCGCCCGAAGATGAGGTCAAGCAAGAGGGGCGAGAGATGAACCTGGAAGTCCGG 530
Db 56 rpLeuArgProGluAspGlyGlyGlnAlaGluGlyAlaGluAspGluLeuGluLeuGln 75

RESULT 4
AAQ74381
ID AAQ74381 PRELIMINARY; PRT; 117 AA.
AC AAQ74381;

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DT 23-APR-2004 (TrEMBLrel. 27, Created)
DT 23-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 23-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ghrelin.
GN GHRL.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14736731;
RA Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
RA Suomi S., Hansen B.C.;
RT "Characterization of the rhesus monkey ghrelin gene and factors
RT influencing ghrelin gene expression and fasting plasma levels.";
RL Endocrinology 145:2197-2205(2004).
DR EMBL; AY372274; AAQ74837.1; -.
SQ SEQUENCE 117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;

Alignment Scores:
Pred. No.: 6,06e-17 Length: 117
Score: 308.00 Matches: 70
Percent Similarity: 51.06% Conservative: 2
Best Local Similarity: 49.65% Mismatches: 3
Query Match: 29.90% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x AAQ74837 (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCGAGCTCTGCTCTGCGCATGCTCTGCGTGGAGTTG 171
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 172 GCCATGGGAGGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg--Ala----- 35
QY 232 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCCGCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACGTGTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAGAGTTCGAAGAGCCACAGCCAGCTGCGCCGAGCTCTAGCAGGCT 471
Db 36 InGlnArgLysGluSerLysProAlaLysLeuGlnProArgAlaLeuGlyGlyT 56
QY 472 GGCTCCGCGGAGATGAGGTCAACAGAGGGGCGAGAGTGAAGTGAAGTCCGG 530
Db 56 rpLeuArgProGluAspGlyAspGlnAlaGluGlyAlaGluAspGluLeuGluLeuGln 75

RESULT 5
AAQ74837
ID AAQ74837 PRELIMINARY; PRT; 117 AA.
AC AAQ74837;
DT 23-APR-2004 (TrEMBLrel. 27, Created)
DT 23-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 23-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ghrelin.
GN GHRL.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
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RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14736731;
RA Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
RA Suomi S., Hansen B.C.;
RT "Characterization of the rhesus monkey ghrelin gene and factors
RT influencing ghrelin gene expression and fasting plasma levels.";
RL Endocrinology 145:2197-2205(2004).
DR EMBL; AY372274; AAQ74837.1; -.
SQ SEQUENCE 117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;

Alignment Scores:
Pred. No.: 6,06e-17 Length: 117
Score: 308.00 Matches: 70
Percent Similarity: 51.06% Conservative: 2
Best Local Similarity: 49.65% Mismatches: 3
Query Match: 29.90% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x AAQ74837 (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCGAGCTCTGCTCTGCGCATGCTCTGCGTGGAGTTG 171
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 172 GCCATGGGAGGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg--Ala----- 35
QY 232 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCCGCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACGTGTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAGAGTTCGAAGAGCCACAGCCAGCTGCGCCGAGCTCTAGCAGGCT 471
Db 36 InGlnArgLysGluSerLysProAlaLysLeuGlnProArgAlaLeuGlyGlyT 56
QY 472 GGCTCCGCGGAGATGAGGTCAACAGAGGGGCGAGAGTGAAGTGAAGTCCGG 530
Db 56 rpLeuArgProGluAspGlyAspGlnAlaGluGlyAlaGluAspGluLeuGluLeuGln 75

RESULT 6
Q8CH53
ID Q8CH53 PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF442491; AAO06965.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR GO; GO:0050791; P:regulation of physiological process; IEA.
DR InterPro; IPR006737; motilin_asoc.
DR InterPro; IPR006738; motilin_ghrelin.
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InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; Motilin assoc.; 1.
DR Pfam; PF04644; Motilin ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Alignment Scores:
Pred. No.: 2,19E-13 Length: 117
Score: 265.00 Matches: 61
Percent Similarity: 48.23% Conservative: 7
Best Local Similarity: 43.26% Mismatches: 7
Query Match: 25.73% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q8CH53 (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCCTTCCTGCTGGCATGCTCTGGTGACTTG 171
Db 1 MetMetSerSerGlyThrIleCySerLeuLeuLeuLeuValTrpMetAspVal 20
QY 172 GCCATGGCAGGTCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetaAlaGlySerSerPheLeuSerProGluHisGlnLys--Thr----- 35
QY 232 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCGCCATCTCTGGGCTTCTCCAGAGCAGAACAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACCTGTTTCTGGAAGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCCCTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAGAGTCAAGAAAGCCACAGCCAGCTGCAAGCTGAGCCCGAGCTCTAGCAGGT 471
Db 36 InGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuGluGlyt 56
QY 472 GGCTCCCGCCGGAAGATGAGGTCAAGCAGAGAGGGGAGAGTGAAGTGAAGTCCGG 530
Db 56 rpleuHisProAspGlyArgGlyGlnAlaGluGluThrGluGluGluLeuLeuLeuLeuArg 75

RESULT 7
Q811T4 PRELIMINARY; PRT; 86 AA.
ID Q811T4
AC AC
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DE Exon 4-deleted preproghrelin variant.
GN Name=Ghrl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss;
RA Jeffery P.L., Herington A.C., Chopin L.K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV179430; ABO27350.1; -;
DR MGd; MG1:1930008; Ghrl.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005576; Extracellular; IDA.
DR InterPro; IPR006738; motilin ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04644; Motilin ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
SQ SEQUENCE 86 AA; 9758 MW; B913858874770512 CRC64;

Alignment Scores:
Pred. No.: 9.8E-13 Length: 86
Score: 257.00 Matches: 60
Percent Similarity: 46.81% Conservative: 6
Best Local Similarity: 42.55% Mismatches: 9
Query Match: 24.95% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q811T4 (1-86)
QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCCTTCCTGCTGGCATGCTCTGGTGACTTG 171
Db 1 MetLeuSerSerGlyThrIleCySerLeuLeuLeuLeuSerMetLeuTrpMetAspMet 20
QY 172 GCCATGGCAGGTCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetaAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala----- 35
QY 232 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCGCCATCTCTGGGCTTCTCCAGAGCAGAACAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACCTGTTTCTGGAAGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCCCTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAGAGTCAAGAAAGCCACAGCCAGCTGCAAGCTGAGCCCGAGCTCTAGCAGGT 471
Db 36 InGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuGluGlyt 56
QY 472 GGCTCCCGCCGGAAGATGAGGTCAAGCAGAGAGGGGAGAGTGAAGTGAAGTCCGG 530
Db 56 rpleuHisProGluAspArgGlyGlnAlaGluGluThrGluGluGluLeuLeuLeuLeuArg 75

RESULT 8
GHRL_MOUSE STANDARD; PRT; 117 AA.
ID GHRL_MOUSE
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN Name=Ghrl; Synonyms=Mtlrp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RC TISSUE=Stomach;
RA MEDLINE=20389976; PubMed=10930375;
RX Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RL "Mouse mRNA for preproghrelin.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; Tissue=Stomach;
SQ SEQUENCE FROM N.A. (ISOFORM 1);

InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; Motilin assoc.; 1.
DR Pfam; PF04644; Motilin ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Alignment Scores:
Pred. No.: 2,19E-13 Length: 117
Score: 265.00 Matches: 61
Percent Similarity: 48.23% Conservative: 7
Best Local Similarity: 43.26% Mismatches: 7
Query Match: 25.73% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q8CH53 (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCCTTCCTGGCATGCTCTGGTGACTTG 171
Db 1 MetMetSerSerGlyThrIleCySerLeuLeuLeuLeuValTrpMetAspVal 20
QY 172 GCCATGGCAGGTCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetaAlaGlySerSerPheLeuSerProGluHisGlnLys--Thr----- 35
QY 232 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCGCCATCTCTGGGCTTCTCCAGAGCAGAACAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACCTGTTTCTGGAAGACATGGGGCTTAGAGTCTTAACAGAGCTGTTTCCCTCCCTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAGAGTCAAGAAAGCCACAGCCAGCTGCAAGCTGAGCCCGAGCTCTAGCAGGT 471
Db 36 InGInArgLySGLySerLysProProAlaLysLeuGlnProArgAlaLeuGluGlyT 56
QY 472 GGCTCCCGCCGGAAGATGAGGTCAAGCAGAGAGGGGAGAGTGAAGTGAAGTCCGG 530
Db 56 rpleuHisProAspGlyArgGlyGlnAlaGluGluThrGluGluGluLeuLeuLeuArg 75

RESULT 7
Q811T4 PRELIMINARY; PRT; 86 AA.
ID Q811T4
AC AC
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DE Exon 4-deleted preproghrelin variant.
GN Name=Ghrl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss;
RA Jeffery P.L., Herington A.C., Chopin L.K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV179430; ABO27350.1; -;
DR MGd; MG1:1930008; Ghrl.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005576; Extracellular; IDA.
DR InterPro; IPR006738; motilin ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04644; Motilin ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
SQ SEQUENCE 86 AA; 9758 MW; B913858874770512 CRC64;

Alignment Scores:
Pred. No.: 9.8E-13 Length: 86
Score: 257.00 Matches: 60
Percent Similarity: 46.81% Conservative: 6
Best Local Similarity: 42.55% Mismatches: 9
Query Match: 24.95% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q811T4 (1-86)
QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCCTTCCTGGCATGCTCTGGTGACTTG 171
Db 1 MetMetSerSerGlyThrIleCySerLeuLeuLeuLeuSerMetLeuTrpMetAspMet 20
QY 172 GCCATGGCAGGTCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetaAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala----- 35
QY 232 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCGCCATCTCTGGGCTTCTCCAGAGCAGAACAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACCTGTTTCTGGAAGACATGGGGCTTAGAGTCTTAACAGAGCTGTTTCCCTCCCTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAGAGTCAAGAAAGCCACAGCCAGCTGCAAGCTGAGCCCGAGCTCTAGCAGGT 471
Db 36 InGInArgLySGLySerLysProProAlaLysLeuGlnProArgAlaLeuGluGlyT 56
QY 472 GGCTCCCGCCGGAAGATGAGGTCAAGCAGAGAGGGGAGAGTGAAGTGAAGTCCGG 530
Db 56 rpleuHisProGluAspArgGlyGlnAlaGluGluThrGluGluGluLeuLeuLeuArg 75

RESULT 8
GHRL_MOUSE STANDARD; PRT; 117 AA.
ID GHRL_MOUSE
AC Q9EQX0; Q9WU21;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein).
GN Name=Ghrl; Synonyms=Mtlrp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RC TISSUE=Stomach;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Kojima M.;
RT "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; Tissue=Stomach;
SQ SEQUENCE FROM N.A. (ISOFORM 1);

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Bessel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Simple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangdisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Havaehizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
[5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RA "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122 (2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=O9EOX0-1; Sequence=Displayed;
CC Name=2; Synonyms=del-gln14-ghrelin;
CC IsoId=Q9EOX0-2; Sequence=VSP_003246;
CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
CC -!- SIMILARITY: Belongs to the motilin family.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; AJ234503; CAB46500.1; -;
CC EMBL; AB035701; BAB19046.1; -;
CC EMBL; AB060078; BAB69857.1; -;
CC EMBL; AK008658; BAB25814.1; -;
CC EMBL; AK008960; BAB25934.1; -;
CC MGD; MGI:1930008; Ghrl.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0005576; C:extracellular; IDA.
CC InterPro; IPR006737; motilin assoc

receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.

-!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=Ghrelin;

CC IsoId=Q9BEF8-1; Sequence=Displayed;

CC Name=2; Synonyms=del-Gln14-ghrelin;

CC IsoId=Q9BEF8-2; Sequence=VSP_003244;

CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).

CC -!- SIMILARITY: Belongs to the motilin family.

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CC -----
 CC EMBL; AJ298295; CAC29155.1; -;
 CC EMBL; AJ298296; CAC29156.1; -;
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC Pfam; PF04643; Motilin_assoc; 1.
 CC Pfam; PF04644; Motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD32162; Preproghrelin; 1.
 CC Alternative splicing; Cleavage on pair of basic residues; Hormone;
 CC Lipoprotein; Signal.
 CC SIGNAL 1 23 By similarity.
 CC PEPTIDE 24 51 Ghrelin (By similarity).
 CC PROPEP 52 117 Removed in mature form (By similarity).
 CC LIPID 26 26 O-octanoyl serine (By similarity).
 CC VARSPLOC 37 37 Missing (in isoform 2).
 CC FTid=VSP_003244.
 CC SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Alignment Scores:

Pred. No.: 4.55e-11 Length: 117
 Score: 237.00 Matches: 59
 Percent Similarity: 44.68% Conservative: 4
 Best Local Similarity: 41.84% Mismatches: 12
 Query Match: 23.01% Indels: 66
 DB: 1 Gaps: 1

US-10-659-782A-11 (1-579) x GHRL_CANFA (1-117)

QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCTCTCTCGCATGCTCTGGCTGGACTTG 171
 Db 1 MetProSerLeuGlyThrMetCysSerLeuLeuPheSerValLeuTrpValAspLeu 20
 QY 172 GCCATGGCAGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCC 231
 Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGln--Lys----- 34
 QY 232 CACAAAGCCCAATGTTGTTCCAGCCCTGCCACTTAGCAACACGACTCTGTGACCTGGAG 291
 Db 34 ----- 34
 QY 292 CAGCAGGCCATCTCTGGGCTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 351
 Db 34 ----- 34
 QY 352 CTCAGTGTCTTCTGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCC 411
 Db 35 -----LeuG 36
 QY 412 AGCAGAGAAAGGACTCGAAGAGCCACAGCCAGCTGACCCCGAGCTCTAGCAGCT 471
 Db 36 InGlnArgLysGluSerLysProAlaLysLeuGlnProArgAlaLeuGluArg 56
 QY 472 GGCCTCCCGCCGAGAGTGGAGTCAAGCAGAGAGGCGAGAGGATGAAGTGAAGTCCGG 530
 Db 56 erLeuGlyProGluAspThrSerGlnValGluGlnAlaGluAspGluLeuGluArg 75

RESULT 12

GHRL_PIG

ID GHRL_PIG STANDARD; PRT; 118 AA.

AC Q9GK75; Q9BDG8; Q9GK74;

DT 28-FEB-2003 (Rel. 41, Created)

Db 36 InGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuGluGlys 56
 QY 472 GGCCTCCCGCCGAGAGTGGAGTCAAGCAGAGGCGAGAGGATGAAGTGAAGTCCGG 530
 Db 56 erLeuGlyProGluAspThrSerGlnValGluGlnAlaGluAspGluLeuGluArg 75

RESULT 11

BAC75929

ID BAC75929 PRELIMINARY; PRT; 117 AA.

AC BAC75929;

DT 02-MAR-2004 (TREMELrel. 27, Created)

DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)

DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)

DE Preproghrelin precursor.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Stomach;

RA Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;

RT "dog ghrelin";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB060700; BAC75929.1; -;

KW SIGNAL.

FT SIGNAL 1 23 Potential.

FT CHAIN 24 51 Ghrelin.

SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;

Alignment Scores:

Pred. No.: 4.55e-11 Length: 117
 Score: 237.00 Matches: 59
 Percent Similarity: 44.68% Conservative: 4
 Best Local Similarity: 41.84% Mismatches: 12
 Query Match: 23.01% Indels: 66
 DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x BAC75929 (1-117)

QY 112 ATGCCCTCCCGAGGACCGTCTGCAGCTCTCTCGCATGCTCTGGCTGGACTTG 171
 Db 1 MetProSerLeuGlyThrMetCysSerLeuLeuPheSerValLeuTrpValAspLeu 20
 QY 172 GCCATGGCAGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCC 231
 Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGln--Lys----- 34
 QY 232 CACAAAGCCCAATGTTGTTCCAGCCCTGCCACTTAGCAACACGACTCTGTGACCTGGAG 291
 Db 34 ----- 34
 QY 292 CAGCAGGCCATCTCTGGGCTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 351
 Db 34 ----- 34
 QY 352 CTCAGTGTCTTCTGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCC 411
 Db 35 -----LeuG 36
 QY 412 AGCAGAGAAAGGACTCGAAGAGCCACAGCCAGCTGACCCCGAGCTCTAGCAGCT 471
 Db 36 InGlnArgLysGluSerLysProAlaLysLeuGlnProArgAlaLeuGluArg 56
 QY 472 GGCCTCCCGCCGAGAGTGGAGTCAAGCAGAGAGGCGAGAGGATGAAGTGAAGTCCGG 530
 Db 56 erLeuGlyProGluAspThrSerGlnValGluGlnAlaGluAspGluLeuGluArg 75

DR pfam: PF04644; Motilin ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 6979 MW; 55D3713C50144D5 CRC64;

Alignment Scores:

Pred. No.:	1.4e-06	Length:	65
Score:	182.50	Matches:	48
Percent Similarity:	42.64%	Conservative:	7
Best Local Similarity:	37.21%	Mismatches:	7
Query Match:	17.72%	Indels:	67
DB:	2	Gaps:	2

US-10-659-782A-11 (1-579) x Q6TGF0 (1-65)

QY	124	GGGACCGCTGCGAGCCTCTGCTCTCGGCATGCTCTGGCTG---GACTTGGCCATGGCA	180
Db	2	GlyThrIleCysSerLeuLeuLeuSerValLeuLeuMetAlaAspLeuAlaMetAla	21
QY	181	GGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCCAACAAAGCC	240
Db	22	GlySerSerPheLeuSerProGluHisGlnLysValGln--Gln-----	35
QY	241	CCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAGCAGACGCC	300
Db	35	-----	35
QY	301	CATCTCTGGGCTTACGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGACCTCACTGT	360
Db	35	-----	35
QY	361	TCTGGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCCAGCAGAGAA	420
Db	36	-----ArgL 37	
QY	421	AGGAGTCGAAGAGCCACCAAGCTGCAGCCCGAGCTCTAGCAGGCTGGCTCCGCC	480
Db	37	YsGluSerLysLysProAlaLysLeuLysProArgAlaLeuGluGlyTrpLeuGlyP	57
QY	481	CGGAAGATGGAGGTCAAGCAGAA	503
Db	57	roGluAspSerGlyGluValGlu	64

Search completed: February 1, 2005, 13:28:11
Job time : 164.5 secs

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